

CATALOG DOCUMENTATION  
EMAP-ESTUARIES PROGRAM LEVEL DATABASE  
1991 VIRGINIAN PROVINCE  
BENTHIC COMMUNITY DATA

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1. DATA SET IDENTIFICATION

1.1 Title of Catalog document

EMAP-Estuaries Program Level Database  
1991 Virginian Province  
Benthic Community Data Summarized by Station

1.2 Authors of the Catalog entry

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1.3 Catalog revision date

28 March 1996

1.4 Data set name

BENTHOS

## 1.5 Task Group

Estuaries

## 1.6 Data set identification code

00029

## 1.7 Version

001

## 1.8 Requested Acknowledgment

If you plan to publish these data in any way, EPA requires a standard statement for work it has supported:

"Although the data described in this article have been funded wholly or in part by the U. S. Environmental Protection Agency through its EMAP-Estuaries Program, it has not been subjected to Agency review, and therefore does not necessarily reflect the views of the Agency and no official endorsement should be inferred."

## 2. INVESTIGATOR INFORMATION

### 2.1 Principal Investigator

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### 2.2. Investigation Participant-Sample Collection

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### 2.3 Principal Investigator-Sample Processing

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## 3. DATA SET ABSTRACT

### 3.1 Abstract of the Data Set

The BENTHOS data set summarizes at the community level the data collected from the benthic grabs taken at each station. Three benthic samples for taxon identification were generally collected at each station. A total and mean count of taxa and individuals were calculated for all taxa and infaunal and epifaunal taxa. The total and mean biomass and mean moisture and silt/clay content are recorded for each station. Field data were averaged to generate the mean grab penetration depth, while mean depth to the Redox Potential Discontinuity layer were not included.

Physical constraints or quality assurance problems precluded the collection or analysis of all samples at a few stations. The total

number of grabs collected at a station which passed Quality Assurance/Quality Control (QA/QC) procedures for collection, shipment and analysis is reported.

### 3.2 Keywords for the Data Set

Benthic Biomass, Benthic Species, Benthic Taxa, Epifaunal Species, Grab Penetration Depth, Infaunal Species, Mean Species Abundance, Moisture, Number of Species, Silt/clay, Species Abundance, Taxa Abundance, Total Species Abundance

## 4. OBJECTIVES AND INTRODUCTION

### 4.1 Program Objective

The Environmental Monitoring and Assessment Program (EMAP) was designed to periodically estimate the status and trends of the Nation's ecological resources on a regional basis. EMAP provides a strategy to identify and bound the extent, magnitude and location of environmental degradation and improvement on a regional scale based on randomly located station sites. The randomly located stations were called Base Sampling Sites (BASE).

### 4.2 Data Set Objective

The objective of the Benthic Community data set is to provide summary data of the bottom dwelling (benthic) communities at each station sampled in the Virginian Province in 1991.

### 4.3 Data Set Background Information

Benthic invertebrates are important secondary consumers in most estuarine systems, represent the largest living reservoir of organic carbon in many estuarine systems, contain many commercially and recreationally important species and are prey for critical life stages of other commercially and recreationally important species.

Benthic invertebrate assemblages are sensitive to disturbance and stress from both natural and anthropogenic origins because of their taxonomic diversity, wide range of physiological tolerances to stress and multiple feeding modes and trophic levels. The condition of these communities is a reflection of local environmental conditions (since members of benthic assemblages generally have limited mobility). The communities respond to both sediment and water column conditions and contain long-lived species relative to most invertebrate communities in the water column. Consequently, benthic community studies have been used in many regional estuarine monitoring programs and have proven to be an effective indicator for describing the extent and magnitude of pollution impacts in estuarine ecosystems.

Benthic monitoring data describing species composition, abundance and biomass were used as indicators of the biological conditions in the estuaries of the Virginian Province. These descriptions, along with additional measurements in other data sets describing habitat indicators (depth, salinity) and pollution exposure indicators (oxygen concentrations, sediment toxicity, sediment contaminant concentrations) are being used to develop a benthic index of environmental condition for the Province.

#### 4.4 Summary of Investigation Parameters

Benthic species diversity, abundance and biomass were counted or measured from the grabs, generally three, collected at a station. Summary data were calculated from these laboratory data.

### 5. DATA ACQUISITION AND SAMPLING METHODS

#### 5.1 Data Acquisition

##### 5.1.1 Sampling Objective

Collect sediment grab samples suitable for the analysis of benthic assemblages and biomass. Three replicate sediment samples were expected to be taken at each station.

##### 5.1.2 Sample Collection Methods Summary

The grab sampler was lowered through the water column such that travel through the last 5 meters was no faster than 1 m/sec. The grab penetrated the sediment by gravity releasing a trigger allowing the jaws to close. When the grab was pulled from the sediment using the winch, the jaws closed, encapsulating the sediment sample. After the sampler was retrieved, it was lowered into an on-board cradle.

##### 5.1.3 Sampling Start Date

22 July 1991

##### 5.1.4 Sampling End Date

13 September 1991

##### 5.1.5 Platform

Sampling was conducted from 8 m (24 ft), twin-engine Chesapeake style work boats.

##### 5.1.6 Sampling Gear

A 1/25 m<sup>2</sup>, stainless steel, Young-modified Van Veen Grab sampler was used to collect sediment grabs for benthic analyses. This grab sampled a sample area of 440 cm<sup>2</sup> and a maximum depth of penetration in the sediment of 10 cm. Samples were sieved through a 0.5 mm round stainless steel sieve.

##### 5.1.7 Manufacturer of Sampling Equipment

Young's Welding, Sandwich, MA

##### 5.1.8 Key Variables

At the time of sample collection, the number of grabs collected was recorded.

##### 5.1.9 Collection Method Calibration

The sampling gear did not require any calibration. It required inspection for deformities incurred due to mishandling or impact on rocky substrates.

#### 5.1.10 Sample Collection Quality Control

To ensure the integrity of the sediment samples collected, the interior surfaces of the grab sampler (including the underside of the hinged top) were rinsed prior to use to assure that no sediment remained from the previous station. To minimize the effects of bow wave disturbance to surficial sediments, the speed of grab through the water column was reduced as it neared the bottom. To minimize the chance of sampling the exact same location twice, after three (3) grabs were taken, the boat was moved five (5) meters downstream by letting out the appropriate length of anchor line. Sediment grabs used for benthic samples were randomly interspersed with the grabs used for sediment chemistry/toxicity samples.

A successful grab had relatively level, intact sediment over the entire area of the grab and a sediment depth at the center of between 7-10 centimeters. Unacceptable grabs included those: substrates or grossly slumped surfaces. Grabs completely filled to the top, where the sediment was in direct contact with the hinged top, were also unacceptable.

The sieve was inspected immediately following the removal of the sample to ensure no organisms were left clinging to the sieve. Any organisms found were placed in the sample jar. The sieve was also thoroughly scrubbed with a stiff brush between samples.

#### 5.1.11 Sample Collection Method Reference

Strobel, C.J. and S.C. Schimmel. 1991. Environmental Monitoring and Assessment Program - Near Coastal Component: 1991 Virginian Province Component Field Operations and Safety Manual. U.S. EPA NHEERL-AED, Narragansett, RI. June 1991.

#### 5.1.12 Sample Collection Method Deviations

NA

### 5.2 Data Preparation and Sample Processing

#### 5.2.1 Sample Processing Objective

Process sediment samples to accurately identify and enumerate all macrobenthic organisms found to the lowest taxonomic category which was possible.

#### 5.2.2 Sample Processing Methods Summary

##### 5.2.2.1 Field Summary

A clear plastic core was inserted into a random location in the grab. The sediment within the core was extruded into a "Whirl Pack" for benthic grain size analysis.

The sample was processed for benthic community analysis. Each grab was placed separately into a frame holding a 500 um sieve. The sieve was placed into a sieve box containing water from the sampling station. The sieve was agitated to wash away sediments and leave organisms, detritus, sand particles and pebbles larger than 500 um.

This method was used to minimize mechanical damage to fauna. A gentle flow of water over the sample was also acceptable.

The contents on the sieve were gently rinsed, using a funnel, into a bottle or bottles. The sieve was inspected for remaining organisms. These were removed by forceps and placed in the bottle. The volume of sample per sample jar was no more than 700 mL. 100 ml of a magnesium chloride solution was then added to each sample bottle and mixed by inversion to narcotize the organisms, thereby minimizing damage upon fixation. The samples were then set aside in the shade for approximately 30 minutes, after which 100 ml of 100% buffered, Rose Bengal stained stock formalin was added to each sample jar. A teaspoon-full of borax was added to the sample to assure saturation of the buffer, then the jar was filled to the rim with seawater to eliminate any air space (final concentration of approximately 10% formalin). The samples were again mixed by inversion and placed in the dark. After processing each grab, the sieve was vigorously cleaned with water and a brush to prevent cross-contamination of samples.

#### 5.2.2.2 Laboratory Summary

**BENTHIC SAMPLES:** The samples were washed through 500 um mesh sieves.

Benthic fauna were sorted from the sediments, identified to species, if possible, and enumerated. Benthic fauna identified included those commonly termed 'macrofauna', i.e., those metazoan organisms retained by a 0.5 mm mesh sieve. 'Meiofaunal' groups were not identified or enumerated. These groups included: nematodes, ostracods, turbellarians, harpacticoid copepods and foraminifera. In addition to meiofauna, taxonomic groups having only planktonic forms were excluded from the identification process. Examples of these groups were copepods and cladocerans.

Benthic fauna were identified to the lowest practical taxonomic level. Macrobenthos were identified to species, except for the following groups: class anthozoa (class), subclass copepoda (order), phylum nemertinea (phylum), subclass ostracoda (subclass) and class turbellaria (class). For samples collected in low salinity (less than 5 ppt) water, oligochaetes and chironomids were identified to species, where possible. Above 5 ppt salinity, individuals of these groups from higher salinities were not further differentiated.

**BIOMASS:** Identified and counted organisms were grouped by categories of taxonomic and ecological significance to be used in biomass determinations, placed in vials and preserved.

Biomass was determined using formaldehyde dry weight. Soft-bodied organisms and those having significant inorganic body parts were treated separately. The dry weight biomass of soft-bodied organisms was directly measured after drying. However, hard-bodied organisms (e.g., bivalves, gastropods, and echinoderms) were acidified prior to measuring dry weight in order to remove calcium carbonate (bivalves >2 cm in length were shucked rather than acidified). Biomass measurements were made using an analytical balance with an accuracy of 0.1 mg. Biomass was determined as shell-free dry weight after drying to a constant weight at 60 degrees C.

In the data base, biomass data are reported along with an abundance value (the number of organisms included in the sample). Data base records with a biomass value greater than zero but with an abundance equal to zero indicate that organism fragments were included in the sample.

SILT/CLAY: The procedure used to determine per cent silt/clay content is summarized below. The sediment sample was stirred, homogenized in a clean beaker and sieved using a 63 um mesh sieve. The fraction retained on the sieve (> 63 um) was transferred to a tared evaporating dish, dried in an oven and weighed as the sand weight. The filtrate fraction (< 63 um) was transferred to a 1 liter graduated cylinder, shaken to evenly distribute the particles and a set volume removed to a tared evaporating dish. The sample was dried and weighed as the silt/clay weight.

MOISTURE: A summary of the procedure used for the determination of moisture contents follows. The sample was brought to room temperature and homogenized in a beaker. An aliquot of wet sediment was placed in a tared evaporating dish and weighed immediately. The sample was dried and weight again.

### 5.2.3 Sample Processing Method Calibration

NA

### 5.2.4 Sample Processing Quality Control

To ensure that measurements were standardized, biomass measurements were made only after samples had been preserved for a minimum of two months. Samples were not transferred to ethanol prior to sorting.

### 5.2.5 Sample Processing Method Reference

U.S. EPA. 1995. Environmental Monitoring and Assessment Program (EMAP): Laboratory Methods Manual-Estuaries, Volume 1: Biological and Physical Analyses. U.S. Environmental Protection Agency, Office of Research and Development, NHEERL-AED, Narragansett, RI. EPA/620/R-95/008.

### 5.2.6 Sample Processing Method Deviations

To ensure that measurements were standardized, biomass measurements were made only after samples had been preserved for a minimum of two months. Samples were NOT transferred to ethanol prior to sorting.

## 6. DATA ANALYSIS AND MANIPULATIONS

### 6.1 Name of New or Modified Value

BSP_GRAB	Grabs (#) included in Summary Data
BSP_TOT	Total # Benthic Taxa in 'n' Grabs
INF_TOT	Total # Infaunal Taxa in 'n' Grabs
EPI_TOT	Total # Epifaunal Taxa in 'n' Grabs
BSP_MEAN	Mean # Benthic Taxa in 'n' Grabs
INF_MEAN	Mean # Infaunal Taxa in 'n' Grabs
EPI_MEAN	Mean # Epifaunal Taxa in 'n' Grabs
BSP_TABN	Total # Organisms in 'n' Grabs
INF_TABN	Total # Infaunal Organisms in 'n' Grabs

## 6.1 Name of New or Modified Value, continued

EPI_TABN	Total # Epifaunal Organisms in 'n' Grabs
BSP_MABN	Mean # Organisms in 'n' Grabs
INF_MABN	Mean # Infaunal Organisms in 'n' Grabs
EPI_MABN	Mean # Epifaunal Organisms in 'n' Grabs
BIOMMEAN	Mean Biomass (g) of 'n' grabs, all Taxa
BIOM_TOT	Total Biomass (g) of 'n' Grabs, all Taxa
SICL_B_M	Mean Silt/Clay Content (%) in 'n' Cores
MOIST_M	Mean Moisture Content (%) in 'n' Cores
GRBDEP_M	Grab Penetration: Mean Depth (mm)

## 6.2 Data Manipulation Description

Measurements on a 'per grab' basis were received from taxonomic laboratories. Values in this data set were calculated in two (2) ways: 1) Total measurements were summed from replicate measurements for a parameter over 'n' grabs and 2) a mean of the measurement was taken across 'n' replicate values. Generally, total and mean values are based on the collection of three (3) grabs collected at a station.

## 6.3 Data Manipulation Examples

### 6.3.1 Total value for biomass (BIOM\_TOT) and abundances (\*\_TABN)

Replicate values for a parameter are summed across all grabs collected at a station

### 6.3.2 Mean value for biomass (BIOMMEAN) and abundances (\*\_MABN)

Replicate values for a parameter are summed across all grabs collected at a station and divided by 'n' grabs collected at a station

### 6.3.3 Value for total number of taxon (\*\_TOT) identified at a station

Those codes were excluded which were not considered unique species collected at a station. This meant that if a species code was flagged as not unique in one grab, it was considered not unique in all grabs at a station.

Once all non-unique species codes were excluded, the codes at a station were sorted alphabetically, regardless of grab. The total number of unique species codes were then counted.

### 6.3.4 Value for mean number of taxon (\*\_MEAN) collected at a station

Those taxon codes were excluded which were not considered a unique species identified in a grab.

Once all non-unique species codes were excluded, the codes in a grab were sorted alphabetically. The total number of unique species codes in a grab were then counted. The total numbers for each grab were summed and divided by 'n' grabs for a station.

### 6.3.5 The sediment water content (moisture) calculation was as follows:

$$\% \text{ water} = \frac{(\text{wet wt} - \text{tare}) - (\text{dry wt.} - \text{tare})}{(\text{wet wt} - \text{tare})} \times 100$$



Correction of the dry weight for salt content was also performed, as appropriate for each sample.

6.3.6 The silt/clay content calculation was:

The silt-clay weight calculation is as follows:

$$\text{Silt-clay weight} = (\text{gross wt.} - \text{tare wt.}) * (\text{total volume in cylinder}) / (\text{sample volume from cylinder})$$

The percent silt-clay calculation is as follows:

$$\% \text{ silt-clay} = \text{silt-clay wt} / (\text{sand wt} + \text{silt-clay wt}) * 100$$

## 7. DATA DESCRIPTION

### 7.1 Description of Parameters

Parameter #	SAS Name	Data Type	Len	Format	Parameter Label
1	STA_NAME	Char	8	8.	The Station Identifier
2	VST_DATE	Num	8	YYMMDD6.	The Date the Sample was Collected
3	BSP_GRAB	Num	8	2.	Grabs (#) included in Summary Data
4	BSP_TOT	Num	8	5.	Total # Benthic Taxa in 'n' Grabs
5	INF_TOT	Num	8	4.	Total # Infaunal Taxa in 'n' Grabs
6	EPI_TOT	Num	8	4.	Total # Epifaunal Taxa in 'n' Grabs
7	BSP_MEAN	Num	8	7.2	Mean # Benthic Taxa in 'n' Grabs
8	INF_MEAN	Num	8	7.2	Mean # Infaunal Taxa in 'n' Grabs
9	EPI_MEAN	Num	8	7.2	Mean # Epifaunal Taxa in 'n' Grabs
10	BSP_TABN	Num	8	5.	Total # Organisms in 'n' Grabs
11	INF_TABN	Num	8	5.	Total # Infaunal Organisms in 'n' Grabs
12	EPI_TABN	Num	8	5.	Total # Epifaunal Organisms in 'n' Grabs
13	BSP_MABN	Num	8	7.2	Mean # Organisms in 'n' Grabs
14	INF_MABN	Num	8	7.2	Mean # Infaunal Organisms in 'n' Grabs
15	EPI_MABN	Num	8	7.2	Mean # Epifaunal Organisms in 'n' Grabs
16	BIOM_TOT	Num	8	8.4	Total Biomass (g) of 'n' Grabs, all Taxa
17	BIOMMEAN	Num	8	8.5	Mean Biomass (g) of 'n' grabs, all Taxa
18	SICL_B_M	Num	8	6.3	Mean Silt/Clay Content (%) in 'n' Cores
19	MOIST_M	Num	8	5.2	Mean Moisture Content (%) in 'n' Cores
20	GRBDEP_M	Num	8	4.	Grab Penetration: Mean Depth (mm)
21	RPDDEP_M	Num	8	3.	Redox Pot'nt'l Discont'y: Mean Depth (mm)

### 7.1.7 Minimum Value in Data Set

BSP_GRAB	3
BSP_TOT	0
INF_TOT	0
EPI_TOT	0
BSP_MEAN	0
INF_MEAN	0
EPI_MEAN	0
BSP_TABN	0
INF_TABN	0
EPI_TABN	0
BSP_MABN	0
INF_MABN	0
EPI_MABN	0
BIOMMEAN	0
BIOM_TOT	0
SICL_B_M	0.391
MOIST_M	13.58
GRBDEP_M	63

### 7.1.7 Maximum Value in Data Set

BSP_GRA	3
BSP_TOT	94
INF_TOT	65
EPI_TOT	32
BSP_MEAN	61.33
INF_MEAN	45.66
EPI_MEAN	18.66
BSP_TABN	15244
INF_TABN	14742
EPI_TABN	2894
BSP_MABN	5081.33
INF_MABN	4914.00
EPI_MABN	964.66
BIOMMEAN	9.31495
BIOM_TOT	27.9448
SICL_B_M	98.178
MOIST_M	81.76
GRBDEP_M	104

## 7.2 Data Record Example

### 7.2.1 Column Names for Example Records

STA_NAME	VST_DATE	BSP_GRAB	BSP_TOT	INF_TOT	EPI_TOT	BSP_MEAN	
INF_MEAN	EPI_MEAN	BSP_TABN	INF_TABN	EPI_TABN	BSP_MABN	INF_MABN	
EPI_MABN	BIOMMEAN	BIOM_TOT	SICL_B_M	MOIST_M	GRBDEP_M	RPDDEP_M	

### 7.2.2 Example Data Records

OBS	STA_NAME	VST_DATE	BSP_GRAB	BSP_TOT	INF_TOT	EPI_TOT	BSP_MEAN	INF_MEAN
1	VA91-261	910803	3	62	45	17	34.33	25.67
2	VA91-262	910815	3	90	60	30	55.00	36.33
3	VA91-263	910803	3	24	18	6	15.33	12.00
4	VA91-265	910818	3	47	41	6	33.00	29.00

### 7.2.2 Example Data Records, continued

OBS	EPI_MEAN	BSP_TABN	INF_TABN
-----	----------	----------	----------

1	8.67	740	590
2	18.67	2237	764
3	3.33	173	138
4	4.00	617	511

OBS	EPI_TABN	BSP_MABN	INF_MABN	EPI_MABN	BIOMMEAN	BIOM_TOT	SICL_B_M
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1	150	246.67	196.67	50.00	0.2697	0.8092	55.98
2	1473	745.67	254.67	491.00	0.4657	1.3970	5.93
3	35	57.67	46.00	11.67	0.0616	0.1848	75.84
4	106	205.67	170.33	35.33	0.7303	2.1908	31.52

OBS	MOIST_M	GRBDEP_M	RPDDEP_M
-----	---------	----------	----------

1	19.62	76	.
2	18.76	71	.
3	53.22	86	.
4	28.14	90	.

## 8. GEOGRAPHIC COVERAGE

### 8.1 Minimum Longitude

-77 Degrees 18 Minutes 58.80 Decimal Seconds

### 8.2 Maximum Longitude

-70 Degrees 01 Minutes 00.00 Decimal Seconds

### 8.3 Minimum Latitude

36 Degrees 56 Minutes 24.60 Decimal Seconds

### 8.4 Maximum Latitude

42 Degrees 08 Minutes 00.00 Decimal Seconds

### 8.5 Name of area or region

Virginian Province

Stations were located in estuaries along the East Coast of the United States from Cape Cod, Massachusetts, to Cape Henry, Virginia, at the mouth of the Chesapeake Bay. The area includes the District of Columbia and the States of Virginia, Maryland, New Jersey, Delaware, Pennsylvania, New York, Connecticut, Rhode Island and Massachusetts.

## 9. QUALITY CONTROL/ QUALITY ASSURANCE

### 9.1 Measurement Quality Objectives

Measurement quality objectives were outlined in the Quality Assurance Project Plan (Valente and Schoenherr, 1991). Accuracy goals are outlined below:

Benthic Community Composition	Accuracy Goal	Precision Goal	Completion Goal
Sorting	10 %		90%
Counting	10 %		90%
Taxonomic Identification	10 %		90%
Biomass		10 %	

## 9.2 Quality Assurance/Control Methods

### 9.2.1 Sample Collection Quality Control

Following sieving, the sieve was carefully inspected to ensure that no organisms remained.

Each crew was visited during the sampling period by the QA Coordinator or Logistics coordinator. Part of the review included observing sample collection procedures to ensure samples were being processed properly.

### 9.2.2 Sample Processing Quality Control

Quality control for processing grab samples involves both sorting and counting check systems. A check on the efficiency of the sorting process was required to document the accuracy of the organism extraction process. Checks on the accuracy of sample counting were conducted in conjunction with taxonomic identification and used the same criteria.

The Quality control check on each technician's efficiency at sorting (i.e., separating organisms from sediment and debris) consists of a independent re-sort by a second, experienced sorter. To pass QC, the sorter's efficiency must be at least 90%, meaning no more than 10% of the organisms in the sample were missed. A minimum of 10 percent of samples processed by a given sorter should be subjected to a QC sort at regular intervals during sample processing. If a sorter fails QC sorts, then all samples processed from the last successful QC check were resorted and any additional organisms found were added to each sample. If QC sorting passes, but some organisms were found, these animals WERE NOT added to the original sample sort.

As organisms were identified and corrected, a voucher specimen collection was compiled. This specimen collection can be used as a quality cross check by sending specimens to a separate laboratory for identification. All specimens were to be taxonomically confirmed by an outside source and any discrepancies resolved. Identification and enumeration accuracy were checked internally by a second taxonomist for at least 10 percent of the samples processed by a given technician. There should be no more than 10 percent total error (for all species) in identification or enumeration in any sample. The same procedures for sample reprocessing that are used for sorting apply to identification and counting.

Biomass determination procedures involve drying and weighing a sample. Duplicate weight measurements by a separate technician were taken before and after drying of 10 % of the samples to control and document the precision of this measurement process. If the two technicians' results differ by more than 10 percent, the source of error was identified and corrected before analysis proceeded. A series of blanks (no less than 5% of the number of samples being processed) were also included in the set of samples being dried as an additional QC check. The weight of

these blanks should have varied by no more than 0.1 mg. If greater variations were found, the balance and the procedures used by the technician in its operation were checked and corrective action taken, if necessary.

### 9.3 Quality Assessment Results

Two QA steps were required by the EMAP-VP 1991 QA Project Plan: in-house QC checks (i.e., resorts, recounts, and ID confirmation) on 10% of each technician's work, and independent verification of species identification. The recounts (multiple types - see Table 7-2) and preliminary species verification were performed by the laboratory performing the analyses. Most of these met the requirements established in the QA Plan. Definitive verification of species identification was performed by an independent laboratory and the results are described below.

A total of 137 specimens collected from oligohaline stations were sent to the Aquatic Resources Center in Franklin, TN for independent taxonomic verification. Eleven (8%) were mis-identified, representing 8 species. The identification of an additional 15 specimens could not be confirmed because of the condition of the specimen (e.g., key taxonomic features missing or destroyed, or male needed for identification and only females sent).

The identification of many of these species is difficult. Misidentified species were closely related taxonomically to the "true" species. In general, the report on species verification was "largely favorable" indicating the analytical laboratory performed well. Suggestions were made regarding identification of tubificid oligochaetes and mollusks prior to the next season.

Table 7-2. Results of recounts performed by the laboratory processing benthic infauna samples in 1991. Approximately 10% of all samples were processed in duplicate.

Measurement	Mean Error	Range of Error
Benthic sorting	4.5%	0 - 20.5%
Species identification and enumeration	2.4%	0 - 14%
Biomass	0.13%	0 - 1.6%
Weighing blanks for biomass	0.0001g	0 - 0.0023g

### 9.4 Unassessed Errors

The methods used to process benthic samples require that a small number of representative specimens of each species be set aside in a taxonomic reference collection. However, the biomass of specimens saved for the reference collection could not be measured or estimated. In most cases, specimens in the reference collection were estimated to represent a small percentage of the total macrofaunal biomass. Nonetheless, the total biomass is underestimated for those samples from which reference specimens were taken.

Total macrofaunal biomass was also potentially underestimated for samples from tidal fresh and oligohaline salinity regions where the number of chironomids or the number of oligochaetes was less than 20. Where oligochaetes and chironomids were present in sufficient numbers (>20), half were mounted on slides to complete taxonomic identifications and half were used for biomass measurements. In those instances where the number of oligochaetes or chironomids was <20, all specimens were mounted for identification and no biomass measurements were made. This procedure generally has a negligible effect on biomass estimates.

An additional source of error results from the process of removing an aliquot of sediment from each grab for grain size analysis. This sample (a 2 cm core) was removed from each grab prior to sieving. No attempt was made to "correct" for the animals potentially lost to this sample.

## 10. DATA ACCESS

### 10.1 Data Access Procedures

Data can be downloaded from the WWW server.

### 10.2 Data Access Restrictions

### 10.3 Data Access Contact Persons

John Paul, Ph.D.  
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(401) 782-3037 (Tel.)  
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Data Librarian EMAP-Estuaries  
U.S. EPA NHEERL-AED  
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(401) 782-3030 (FAX)  
hughes.melissa@epa.gov

### 10.4 Data Set Format

Data can be downloaded in several formats from the web application and web site.

### 10.5 Information Concerning Anonymous FTP

Not accessible

### 10.6 Information Concerning WWW

Data can be downloaded from the WWW server.

### 10.7 EMAP CD-ROM Containing the Data Set

Data not available on CD-ROM.

## 11. REFERENCES

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